WE CLAIM:

1. A method of predicting at least one toxic effect of a compound, comprising:
   (a) obtaining a gene expression profile of a tissue or cell sample exposed to the compound; and
   (b) comparing the gene expression profile to a database comprising substantially all of the data or information of Tables 5A-5LL.

2. A method of claim 1, wherein the gene expression profile obtained from the tissue or cell sample comprises the level of expression for at least one gene.

3. A method of claim 2, wherein the level of expression is compared to a Tox Mean and/or NonTox Mean value in Tables 5A-5LL.

4. A method of claim 3, wherein the level of expression is normalized prior to comparison.

5. A method of claim 1, wherein the database comprises substantially all of the data or information in Tables 5A-5LL.

6. A method of claim 1, wherein the tissue or cell sample is a heart tissue or heart cell sample.

7. A method of predicting at least one toxic effect of a compound, comprising:
   (a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II; wherein differential expression of the genes in Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II is indicative of at least one toxic effect.

8. A method of predicting the progression of a toxic effect of a compound, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II; wherein differential expression of the genes in Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II is indicative of toxicity progression.

9. A method of predicting the cardiotoxicity of a compound, comprising:
(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II; wherein differential expression of the genes in 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II is indicative of cardiotoxicity.

10. A method of identifying an agent that modulates the onset or progression of a toxic response, comprising:
(a) exposing a cell to the agent and a known toxin; and
(b) detecting the agent induced change in the expression level of two or more genes from Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II; wherein differential expression of the genes in Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II, compared to a control, is indicative of toxicity.

11. A method of predicting the cellular pathways that a compound modulates in a cell, comprising:
(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II; wherein differential expression of the genes in Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II is associated the modulation of at least one cellular pathway.

12. The method of any one of claims 7-11, wherein the expression levels of at least 5 genes are detected.

13. The method of any one of claims 7-11, wherein the expression levels of at least 10 genes are detected.

14. The method of any one of claims 7-11, wherein the expression levels of at least 25 genes are detected.

15. The method of any one of claims 7-11, wherein the expression levels of at least 50 genes are detected.

16. The method of any one of claims 7-11, wherein the expression levels of at least 100 genes are detected.

17. The method of any one of claims 7-11, wherein the expression levels of at least 200 genes are detected.

18. The method of any one of claims 7-11, wherein the expression levels of at least 500 genes are detected.

19. The method of any one of claims 7-11, wherein the expression levels of nearly all genes are detected.

20. A method of claim 7 or 8, wherein the effect is selected from the group consisting of myocarditis, arrhythmias, tachycardia, myocardial ischemia, angina, hypertension, hypotension, dyspnea, and cardiogenic shock.

21. A method of claim 9, wherein the cardiotoxicity is associated with at least one heart disease pathology selected from the group consisting of myocarditis, arrhythmias, tachycardia, myocardial ischemia, angina, hypertension, hypotension, dyspnea, and cardiogenic shock.

22. A method of claim 11, wherein the cellular pathway is modulated by a toxin selected from the group consisting of cyclophosphamide, ifosfamide, minoxidil,

hydralazine, BI-QT, clenbuterol, isoproterenol, norepinephrine, epinephrine, adriamycin, amphotericin B, epirubicin, phenylpropanolamine, and rosiglitazone.

23. A set of at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II.

24. A set of probes according to claim 23, wherein the set comprises probes that hybridize to at least 10 genes.

25. A set of probes according to claim 23, wherein the set comprises probes that hybridize to at least 50 genes.

26. A set of probes according to claim 23, wherein the set comprises probes that hybridize to at least 100 genes.

27. A set of probes according to claim 23, wherein the set comprises probes that hybridize to at least 500 genes.

28. A set of probes according to any one of claims 23-27, wherein the probes are attached to a solid support.

29. A set of probes according to claim 28, wherein the solid support is selected from the group consisting of a membrane, a glass support and a silicon support.

30. A solid support comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II.

31. A solid support of claim 30, wherein the solid support is an array comprising at least 10 different oligonucleotides in discrete locations per square centimeter.

32. A solid support of claim 31, wherein the array comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.

33. A solid support of claim 31, wherein the array comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.

34. A solid support of claim 31, wherein the array comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.

35. A computer system comprising:
(a) a database containing information identifying the expression level in a tissue or cell sample exposed to a cardiotoxin of a set of genes comprising at least two genes in Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II; and
(b) a user interface to view the information.

36. A computer system of claim 35, wherein the database further comprises sequence information for the genes.

37. A computer system of claim 35, wherein the database further comprises information identifying the expression level for the set of genes in the tissue or cell sample before exposure to a cardiotoxin.

38. A computer system of claim 35, wherein the database further comprises information identifying the expression level of the set of genes in a tissue or cell sample exposed to at least a second cardiotoxin.

39. A computer system of any of claims 35-38, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

40. A computer system of claim 39, wherein the external database is GenBank.

41. A method of using a computer system of any one of claims 35-38 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 5A-5LL, comprising:
comparing the expression level of at least one gene in Tables 5A-5LL in a tissue or cell exposed to a test agent to the level of expression of the gene in the database.

42. A method of claim 41, wherein the expression levels of at least 10 genes are compared.

43. A method of claim 41, wherein the expression levels of at least 100 genes are compared.

44. A method of claim 41, wherein the expression levels of at least 500 genes are compared.

45. A method of claim 41, further comprising the step of displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level when exposed to a toxin.

46. A method of claim 10, wherein the known toxin is a cardiotoxin.

47. A method of claim 43, wherein the cardiotoxin is selected from the group consisting of cyclophosphamide, ifosfamide, minoxidil, hydralazine, BI-QT, clenbuterol, isoproterenol, norepinephrine, epinephrine, adriamycin, amphotericin B, epirubicin, phenylpropanolamine, and rosiglitazone.

48. A method of any one of claims 7-11, wherein nearly all of the genes in Tables 5A-5LL are detected.

49. A method of claim 48, wherein all of the genes in at least one of Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II are detected.

50. A kit comprising at least one solid support of any one of claims 30-34 packaged with gene expression information for said genes.

51. A kit of claim 50, wherein the gene expression information comprises gene expression levels in a tissue or cell sample exposed to a cardiotoxin.

52. A kit of claim 51, wherein the gene expression information is in an electronic format.

53. A method of any one of claims 7-11, wherein the compound exposure is *in vivo* or *in vitro*.

54. A method of any one of claims 7-11, wherein the level of expression is detected by an amplification or hybridization assay.

55. A method of claim 54, wherein the amplification assay is quantitative or semi-quantitative PCR.

56. A method of claim 54, wherein the hybridization assay is selected from the group consisting of Northern blot, dot or slot blot, nuclease protection and microarray assays.

57. A method of identifying an agent that modulates at least one activity of a protein encoded by a gene in Tables 5C, 5D, 5E, 5F, 5H, 5J, 5L, 5N, 5P, 5R, 5S, 5U, 5W, 5Y, 5AA, 5CC, 5EE, 5GG, 5HH, and 5II comprising:

(a) exposing the protein to the agent; and

(b) assaying at least one activity of said protein.

58. A method of claim 57, wherein the agent is exposed to a cell expressing the protein.

59. A method of claim 58, wherein the cell is exposed to a known toxin.

60. A method of claim 59 wherein the toxin modulates the expression of the protein.

61. A method of predicting at least one toxic effect of a compound, comprising:
(a) obtaining a gene expression profile of a tissue or cell sample exposed to the compound; and
(b) comparing the gene expression profile to a database comprising at least part of the data or information of Tables 5A, 5B, 5G, 5I, 5K, 5M, 5O, 5Q, 5T, 5V, 5X, 5Z, 5BB, 5DD, 5FF, 5JJ, 5KK, and 5LL.

62. A method of claim 61, wherein the gene expression profile obtained from the tissue or cell sample comprises the level of expression for at least one gene.

63. A method of claim 62, wherein the level of expression is compared to a Tox Mean and/or Non-Tox Mean value in Tables 5A, 5B, 5G, 5I, 5K, 5M, 5O, 5Q, 5T, 5V, 5X, 5Z, 5BB, 5DD, 5FF, 5JJ, 5KK, and 5LL.

64. A method of claim 63, wherein the level of expression is normalized prior to comparison.

65. A method of claim 61, wherein the database comprises substantially all of the data or information in Tables 5A, 5B, 5G, 5I, 5K, 5M, 5O, 5Q, 5T, 5V, 5X, 5Z, 5BB, 5DD, 5FF, 5JJ, 5KK, and 5LL.

66. A method of claim 61, wherein the tissue or cell sample is a heart tissue or heart cell sample.